

Function Alignment

Introduction

[Home](#) > [Find Functions](#) > [Function Alignment](#)

Function Alignment

Function Alignment is a tool that lists alignments of functional prediction for genes. It can be accessed via the second-level menu of **Find Functions**, as shown in Figure 1.

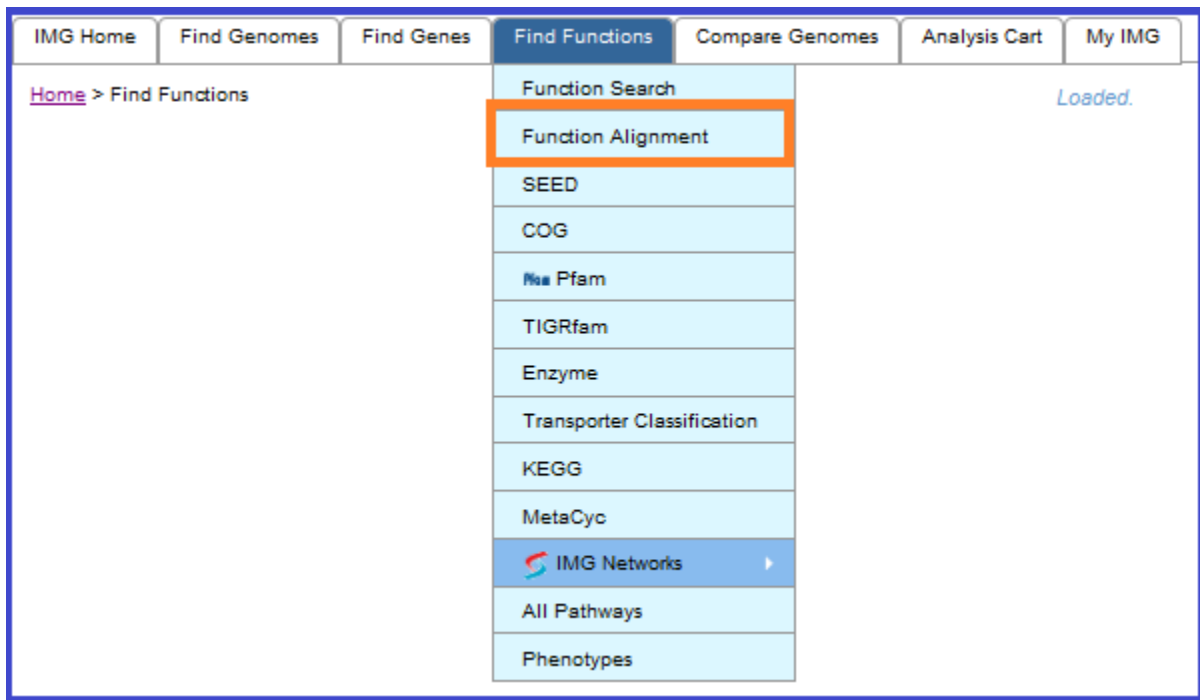


Figure 1: Access Function Search.

Keyword Search

The page of **Function Alignment**, as shown in Figure 2, searches alignments of functional prediction for genes in selected genomes by keyword. User first enters keyword, next selects COG or Pfam or both as filter to look for specific functions and genes.

Home > Find Functions Loaded.

Function Alignment Search

Find alignments in selected functions and genomes by keyword.

Keyword:

Filters:

Genome Filter

Domains: (B)acteria, (A)rchaea, (E)ukarya, (P)lasmsids, (V)iruses.
Genome Completion: [F]inished, [P]ermanent Draft, [D]raft.

Seq. Status: Domain:

☒ List ☐ Tree

- Acidilobus saccharovorans 345-15 (A)[F]
- Aciduliprofundum boonei T469 (A)[D]
- Aciduliprofundum boonei T469 (A)[F]
- Aeropyrum pernix K1 (A)[F]
- Archaeoglobus fulgidus DSM 4304 (A)[F]
- Archaeoglobus profundus DSM 5631 (A)[F]
- Caldivirga maquilensis IC-167 (A)[F]
- Candidatus Korarchaeum cryptofilum OPF8 (A)[F]
- Candidatus Methanoregula boonei 6A8 (A)[F]
- Cenarchaeum symbiosum A (A)[F]

Examples

- "Shikimate kinase" as "All Function names" search will get the alignment of functional prediction for genes with matching COG or Pfam functions.
- "COG3729" as "COG" search will retrieve the alignment of functional prediction for genes that correspond with COG3729.
- "pfam10261" as "Pfam" search retrieve the alignment of functional prediction for genes that have the pfam domain hits *pfam10261*.
- Prefixes for cog and pfam are assumed, above can be shorten to "3729" or "10261".

Figure 2: Function Alignment Search.

The result page is split into two parts through tab view: COG and Pfam. If the Function Alignment search involves only one type of function, then either COG or Pfam tab view is displayed, not both (Figure 1).

All Function Alignment Search Results

COG

Pfam

Search column: COG ID Search term:

Export

Page 1 of 1 << first < prev 1 next > last >> All

Column Selector

Gene Object ID	COG ID	COG Name	Consensus Sequence Length	Percent Identity	Query Start	Query End	Alignment On Query Gene	Bit Score	Genome
640868797	COG0703	[E] Amino acid transport and metabolism Shikimate kinase	172	40.48	1	166		154	Candidatus Methanoregula boonei 6A8
637702022	COG0703	Shikimate kinase	172	42.17	1	164		154	Methanosarcina barkeri fusaro
640115988	COG0703	Shikimate kinase	172	44.44	1	160		148	Methanoculleus marisnigri JR1
643571201	COG0703	Shikimate kinase	172	40.94	1	169		146	Methanosphaeula palustris F1-9c
640868484	COG0703	Shikimate kinase	172	37.8	1	161		144	Candidatus Methanoregula boonei 6A8
637897466	COG0703	Shikimate kinase	172	34.91	1	166		137	Methanospirillum hungatei JF-1
637958615	COG0703	Shikimate kinase	172	35.93	1	164		134	Methanococcoides burtonii DSM 6242
648055184	COG0703	Shikimate kinase	172	32.75	1	169		133	Methanohalobium vestitatum Z-7303
646707050	COG0703	Shikimate kinase	172	34.76	1	162		132	Methanohalophilus mahii DSM 5219

Figure 3: Function Alignments Search Results.

User can also access Function Alignment from pages of **Gene Cart** and **Function Cart**.

Genome Filter

The Genome Filter is provided to limit the scope of search. The search is conducted on the genomes that user has saved through the **Genome Browser**. If user saves nothing, by default, it's all genomes in IMG database. However, user can override the selection via the **Genome Filter** provided in the page.

For more information about **Genome Filter**, go to “[Home > User Guide > Site Map](#)”.

Search Specifications

All searches are case-insensitive. The “list” search has to be separated by “,”.

User can use a percent sign (%) as a wildcard in the middle of a keyword. The results will include any genes with zero or more additional characters at that position. For example, "hydro%ase" in "Gene Product Name" will get results with "hydrolase" and "hydrogenase", etc. If user wants only a single character of the keyword to be variable, type an underscore (_) in that position. Searching for "hydro_ase" will get results with "hydrolase," not "hydrogenase."